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ABSTRACT

The present invention recognizes that identifying genes expressed during developmental processes, stress responses, and disease states can advance understanding of these biological functions, and can contribute to identifying targets for therapeutic drugs. In addition, the present invention recognizes that rapid and reliable profiling of genetic variations, such as mutations and SNPs, is of increasing importance to diagnostics, prognostics, forensics, heredity determinations, and pharmacogenetics. One aspect of the present invention provides a method of identifying one or more nucleic acid molecules that are expressed under a given set of conditions based on their complementarity to known sequences, or one or more mutations or SNPs in a population of nucleic acid molecules. The method includes: contacting at least one probe nucleic acid molecule with a survey population of nucleic acid molecules under conditions that promote nucleic acid hybridization to generate a probe-survey population mixture of nucleic acid molecules, treating the probe-survey population mixture of nucleic acid molecules with a nucleolytic activity, such that nucleolytic activity-sensitive nucleic acid molecules are digested, and contacting the resulting mixture of nucleolytic activity-protected nucleic acid molecules with a solid support comprising one or more attached nucleic acid molecules to generate attached nucleic acid molecule/nucleolytic activity-protected nucleic acid molecule complexes, and identifying one or more of the attached nucleic acid molecules or one or more of the nucleolytic activity-protected nucleic acid molecules in one or more attached nucleic acid molecule/nucleolytic activity-protected nucleic acid molecule complexes.